

**BLAST Basic Local Alignment Search Tool**

Job Title: Nucleotide sequence (21 letters)

- Your search parameters were adjusted to search for a short input sequence.

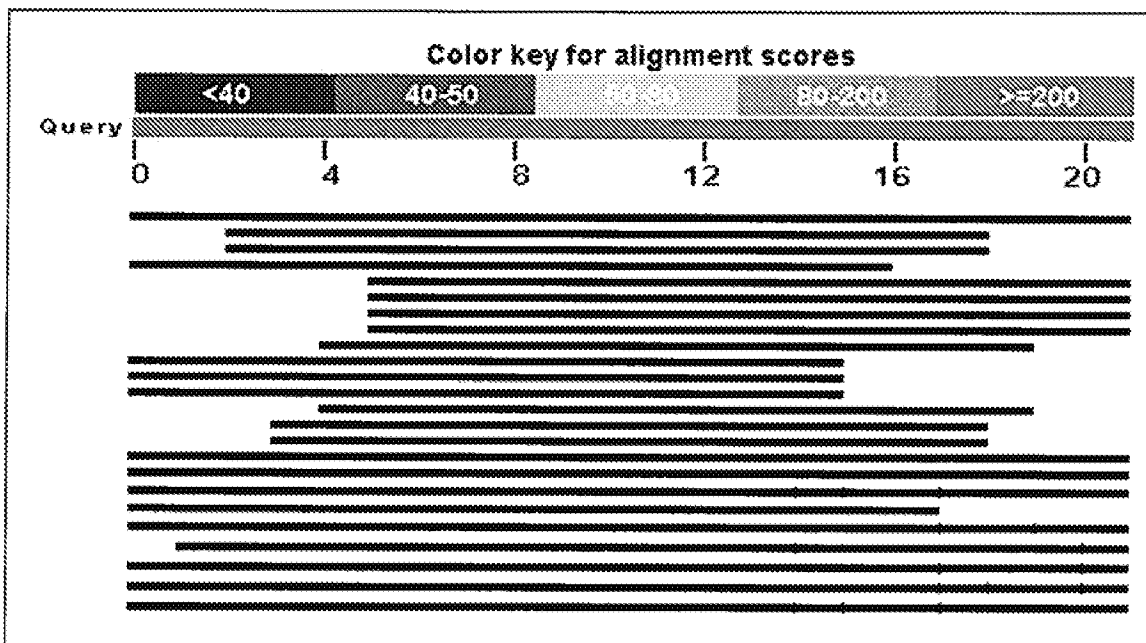
Please, try our new design!

**BLASTN 2.2.18+**






Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 9HCHHWH3015 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= Length=21












































































☐ Designing or Testing PCR Primers? Try your s**Distribution of 1401 Blast Hits on the Query Sequence**

[REDACTED]

Distance tree of results NEWLegend for links to other resources:  UniGene  GEO  Gene  Structure  Map**Sequences producing significant alignments:**

(Click headers to sort columns)

**Transcripts**

|                            |  |      |      |      |       |      |   |
|----------------------------|--|------|------|------|-------|------|---|
| gi 113722118 NM_000372.4   | Homo sapiens tyrosinase (oculocutaneous albinism IA) (TYR), mRNA   | 42.1 | 42.1 | 100% | 0.005 | 100% |                |
| gi 148806860 NR_003571.1   | Homo sapiens protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) pseudogene (LOC728758) on chromosome 15     | 32.2 | 32.2 | 76%  | 4.7   | 100% |                |
| gi 4809273 NM_001154.2     | Homo sapiens annexin A5 (ANXA5), mRNA  | 32.2 | 32.2 | 76%  | 4.7   | 100% |                |
| gi 14150142 NM_032347.1    | Homo sapiens zinc finger protein 397 (ZNF397), mRNA  | 32.2 | 32.2 | 76%  | 4.7   | 100% |                |
| gi 65508003 NM_024426.3    | Homo sapiens Wilms tumor 1 (WT1), transcript variant D, mRNA   | 32.2 | 32.2 | 76%  | 4.7   | 100% |                |
| gi 65507907 NM_024425.2    | Homo sapiens Wilms tumor 1 (WT1), transcript variant C, mRNA   | 32.2 | 32.2 | 76%  | 4.7   | 100% |            |
| gi 65507816 NM_024424.2    | Homo sapiens Wilms tumor 1 (WT1), transcript variant B, mRNA   | 32.2 | 32.2 | 76%  | 4.7   | 100% |      |
| gi 65507713 NM_000378.3    | Homo sapiens Wilms tumor 1 (WT1), transcript variant A, mRNA   | 32.2 | 32.2 | 76%  | 4.7   | 100% |      |
| gi 98986451 NM_023075.4    | Homo sapiens metallophosphoesterase 1 (MPPE1), mRNA  | 30.2 | 30.2 | 71%  | 19    | 100% |      |
| gi 46488931 NM_000629.2    | Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA  | 30.2 | 30.2 | 71%  | 19    | 100% |      |
| gi 62388889 NM_001014797.1 | Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), transcript variant 1, mRNA | 30.2 | 30.2 | 71%  | 19    | 100% |      |
| gi 26638649 NM_002247.2    | Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), transcript variant 2, mRNA | 30.2 | 30.2 | 71%  | 19    | 100% |      |
| gi 24307982 NM_015050.1    | Homo sapiens KIAA0082 (KIAA0082), mRNA   | 30.2 | 30.2 | 71%  | 19    | 100% |      |
| gi 56549110 NM_001008213.1 | Homo sapiens optineurin (OPTN), transcript variant 4, mRNA   | 30.2 | 30.2 | 71%  | 19    | 100% |      |
| gi 56549108 NM_001008212.1 | Homo sapiens optineurin (OPTN), transcript variant 3, mRNA   | 30.2 | 30.2 | 71%  | 19    | 100% |      |


**Genomic sequences [show first]**

|                             |                            |      |     |      |       |      |
|-----------------------------|----------------------------|------|-----|------|-------|------|
| gi 157812179 NW_001838029.2 | Homo sapiens chromosome 11 | 42.1 | 122 | 100% | 0.005 | 100% |
|-----------------------------|----------------------------|------|-----|------|-------|------|

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## Alignments


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>gi|113722118|ref|NM\_000372.4|  Homo sapiens tyrosinase (oculocutaneous albinis  
Length=2082

GENE ID: 7299 TYR | tyrosinase (oculocutaneous albinism IA) [Homo sapiens]  
(Over 100 PubMed links)

Score = 42.1 bits (21), Expect = 0.005  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus


```
Query 1 AATCCTGGAAACCATGACAAA 21
      |||
Sbjct 980 AATCCTGGAAACCATGACAAA 1000
```

>gi|148806860|ref|NR\_003571.1|  Homo sapiens protein (peptidylprolyl cis/trans isom  
4 (parvulin) pseudogene (LOC728758) on chromosome  
15  
Length=2366

GENE ID: 728758 hCG\_1789710 | protein (peptidylprolyl cis/trans isomerase)  
NIMA-interacting, 4 (parvulin) pseudogene [Homo sapiens]  
(10 or fewer PubMed links)


Score = 32.2 bits (16), Expect = 4.7  
Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

```
Query 3 TCCTGGAAACCATGAC 18
      |||
Sbjct 252 TCCTGGAAACCATGAC 237
```

>gi|4809273|ref|NM\_001154.2|  Homo sapiens annexin A5 (ANXA5), mRNA  
Length=1630

Score = 32.2 bits (16), Expect = 4.7  
Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

```
Query 3 TCCTGGAAACCATGAC 18
      |||
Sbjct 1021 TCCTGGAAACCATGAC 1006
```

>gi|14150142|ref|NM\_032347.1|  Homo sapiens zinc finger protein 397 (ZNF397), m  
Length=1439

GENE ID: 84307 ZNF397 | zinc finger protein 397 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 4.7

USSN 10/738,413

EXHIBIT 6

Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Plus

Query 1 AATCCTGGAAACCATG 16  
Sbjct 659 AATCCTGGAAACCATG 674

>gi|65508003|ref|NM\_024426.3| **U E G M** Homo sapiens Wilms tumor 1 (WT1), transcript var  
Length=3029

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7  
Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21  
Sbjct 2192 TGGAAACCATGACAAA 2177

>gi|65507907|ref|NM\_024425.2| **U E G M** Homo sapiens Wilms tumor 1 (WT1), transcript var  
Length=2978

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7  
Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21  
Sbjct 2141 TGGAAACCATGACAAA 2126

>gi|65507816|ref|NM\_024424.2| **U E G M** Homo sapiens Wilms tumor 1 (WT1), transcript var  
Length=3020

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7  
Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21  
Sbjct 2183 TGGAAACCATGACAAA 2168

>gi|65507713|ref|NM\_000376.3| **U E G M** Homo sapiens Wilms tumor 1 (WT1), transcript var  
Length=2969

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7  
Identities = 16/16 (100%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21  
Sbjct 2132 TGGAAACCATGACAAA 2117

>gi|98986451|ref|NM\_023075.4| **U E G M** Homo sapiens metallophosphoesterase 1 (MPPE1), m  
Length=2806

GENE ID: 65258 MPPE1 | metallophosphoesterase 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 19

USSN 10/738,413

EXHIBIT 6

Identities = 15/15 (100%); Gaps = 0/15 (0%)  
Strand=Plus/Plus

|       |      |                 |      |
|-------|------|-----------------|------|
| Query | 5    | CTGGAAACCATGACA | 19   |
|       |      |                 |      |
| Sbjct | 1105 | CTGGAAACCATGACA | 1119 |